OIPE

ENTERED

Input Set: I477392.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

```
 1   <110> APPLICANT: Heintz, Nicholas
 2               Houchens, Christopher
 3   <120> TITLE OF INVENTION: RIP60 Nucleic Acid and Polypeptide
 4               Sequences and Uses Therefor
 5   <130> FILE REFERENCE: V0139/7038 (HCL/MAT)
 6   <140> CURRENT APPLICATION NUMBER: US/09/477,392
 7   <141> CURRENT FILING DATE: 2000-01-04
 8   <150> EARLIER APPLICATION NUMBER: US 60/114,745
 9   <151> EARLIER FILING DATE: 1999-01-04
10   <150> EARLIER APPLICATION NUMBER: US 60/114,743
11   <151> EARLIER FILING DATE: 1999-01-04
12   <160> NUMBER OF SEQ ID NOS: 68
13   <170> SOFTWARE: FastSEQ for Windows Version 3.0
14   <210> SEQ ID NO 1
15   <211> LENGTH: 2954
16   <212> TYPE: DNA
17   <213> ORGANISM: Homo Sapiens
18   <220> FEATURE:
19   <221> NAME/KEY: CDS
20   <222> LOCATION: (130)...(1831)
21   <400> SEQUENCE: 1
22         cgctgtttgt ccagcttctc agagttgctg tgcagctcgg atgtggcata ggaaacagca      60
23         gacacaggga gagggcagca taaggcactg tagggagcag tggccacatt ttctgcagag     120
24         gaagaaccg atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg ggc ctg     171
25                   Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu
26                    1               5                  10
27         gcc cag ccc cga ctc ctt tct ggg ccc tcc cag gag tca ccc cag acc     219
28         Ala Gln Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr
29          15                20                  25                  30
30         ctg ggg aag gag tcc cgc ggg ctg agg caa caa ggc acg tca gtg gcc     267
31         Leu Gly Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala
32                            35                  40                  45
33         cag tct ggt gcc caa gcc cca ggc agg gcc cat cgc tgt gcc cac tgt     315
34         Gln Ser Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys
35                            50                  55                  60
36         cga agg cac ttc cct ggc tgg gtg gct ctg tgg ctt cac acc cgc cgg     363
37         Arg Arg His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg
38                            65                  70                  75
39         tgc cag gcc cgg ctg ccc ttg ccc tgc cct gag tgt ggc cgt cgc ttt     411
40         Cys Gln Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe
41                  80                  85                  90
42         cgc cat gcc ccc ttc tta gca ctg cac cgc cag gtc cat gct gct gcc     459
43         Arg His Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala
44          95                 100                 105                 110
```

```
45          acc cca gac ctg ggc ttt gcc tgc cac ctc tgt ggg cag agc ttc cga        507
46          Thr Pro Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg
47                      115                 120                 125
48          ggc tgg gtg gcc ctg gtt ctg cat ctg ctg gcc cat tca gct gca aag        555
49          Gly Trp Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys
50                      130                 135                 140
51          caa ccc atc gct tgt ccc aaa tgc gag aga cgc ttc tgg cga cga aag        603
52          Gln Pro Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys
53                      145                 150                 155
54          cag ctt cga gct cat ctg cgg cgg tgc cac cct ccc gcc ccg gag gcc        651
55          Gln Leu Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala
56                160                 165                 170
57          cgg ccc ttc ata tgc ggc aac tgt ggc cgg agc ttt gcc cag tgg gac        699
58          Arg Pro Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp
59          175                 180                 185                 190
60          cag cta gtt gcc cac aag cgg gtg cac gta gct gag gcc ctg gag gag        747
61          Gln Leu Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu
62                      195                 200                 205
63          gcc gca gcc aag gct ctg ggg ccc cgg ccc agg ggc cgc ccc gcg gtg        795
64          Ala Ala Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val
65                      210                 215                 220
66          acc gcc ccc cgg ccc ggt gga gat gcc gtc gac cgc ccc ttc cag tgt        843
67          Thr Ala Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys
68                      225                 230                 235
69          gcc tgt tgt ggc aag cgc ttc cgg cac aag ccc aac ttg atc gct cac        891
70          Ala Cys Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His
71                240                 245                 250
72          cgc cgc gtg cac acg ggc gag cgg ccc cac cag tgc ccc gag tgc ggg        939
73          Arg Arg Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly
74          255                 260                 265                 270
75          aag cgc ttt acc aat aag ccc tat ctg act tcg cac cgg cgc atc cac        987
76          Lys Arg Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His
77                      275                 280                 285
78          acc ggc gag aag ccc tac ccg tgc aaa gag tgc ggc cgc cgc ttc cgg       1035
79          Thr Gly Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg
80                      290                 295                 300
81          cac aaa ccc aac ctg ctg tct cac agc aag att cac aag cga tcc gag       1083
82          His Lys Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu
83                      305                 310                 315
84          ggg tcg gcc cag gcc gcc ccc ggc ccg ggg agc ccc cag ctg cca gcc       1131
85          Gly Ser Ala Gln Ala Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala
86                      320                 325                 330
87          ggc ccc cag gag tcc gcg gcc gag ccc acc ccg gcg gta cct ctg aaa       1179
88          Gly Pro Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys
89          335                 340                 345                 350
90          ccg gcc cag gag ccg ccg cca ggg gcc ccg cca gag cac ccg cag gac       1227
91          Pro Ala Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp
92                      355                 360                 365
93          ccg atc gaa gcc ccc ccc tcc ctc tac agc tgc gac gac tgc ggc agg       1275
94          Pro Ile Glu Ala Pro Pro Ser Leu Tyr Ser Cys Asp Asp Cys Gly Arg
```

```
 95                     370              375                380
 96          agc ttc cgg ctg gag cgc ttc ctg cgg gcc cac cag cgg cac gac acc    1323
 97          Ser Phe Arg Leu Glu Arg Phe Leu Arg Ala His Gln Arg His Asp Thr
 98                     385              390                395
 99          ggg gag cgg ccc ttc acc tgc gcc gag tgc ggg aag aac ttc ggc aag    1371
100          Gly Glu Arg Pro Phe Thr Cys Ala Glu Cys Gly Lys Asn Phe Gly Lys
101                     400              405                410
102          aag acg cac ctg gtg gcg cac tcg ccg gtg cac tcc ggc gag cgg ccc    1419
103          Lys Thr His Leu Val Ala His Ser Pro Val His Ser Gly Glu Arg Pro
104          415                420                425                430
105          ttc gcc tgc gag gag tgc ggc cgc cgc ttc tcc cag ggc agc cat ctg    1467
106          Phe Ala Cys Glu Glu Cys Gly Arg Arg Phe Ser Gln Gly Ser His Leu
107                     435              440                445
108          gcg gcg cat cgg ccg gac cac gcc ccc gat cgg ccc ttc gtg tgt ccc    1515
109          Ala Ala His Arg Pro Asp His Ala Pro Asp Arg Pro Phe Val Cys Pro
110                     450              455                460
111          gac tgc ggc aag gcc ttc cgc cac aaa ccc tac ctg gcg cgg cac cgg    1563
112          Asp Cys Gly Lys Ala Phe Arg His Lys Pro Tyr Leu Ala Arg His Arg
113                     465              470                475
114          cgc atc cac acc ggc gag aag ccc tac gtc tgc ccc gac tgc ggc aaa    1611
115          Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys
116          480                485                490
117          gcc ttc agc cag aag tcc aac ctg gtg tcg cac cgg cgc atc cac acg    1659
118          Ala Phe Ser Gln Lys Ser Asn Leu Val Ser His Arg Arg Ile His Thr
119          495                500                505                510
120          ggc gag cgg ccc tac gcc tgt ccc gac tgc gac cgc agc ttc agc cag    1707
121          Gly Glu Arg Pro Tyr Ala Cys Pro Asp Cys Asp Arg Ser Phe Ser Gln
122                     515              520                525
123          aag tcc aac ctc atc acc cac cgc aag agc cac atc cgg gac ggc gcc    1755
124          Lys Ser Asn Leu Ile Thr His Arg Lys Ser His Ile Arg Asp Gly Ala
125                     530              535                540
126          ttc tgc tgt gcc atc tgt ggc cag acc ttc gac gac gag gag aga ctc    1803
127          Phe Cys Cys Ala Ile Cys Gly Gln Thr Phe Asp Asp Glu Glu Arg Leu
128                     545              550                555
129          ctg gcc cac cag aag aag cac gat gtc t gagacggtgg gcggggccgt         1851
130          Leu Ala His Gln Lys Lys His Asp Val
131          560              565
132          gttggctgag agagggctgg ggtccttcgt ggtgggagtc gcagtgggct gggggtgcct   1911
133          gcctagtgct ggagtagggg acaatgggaa tcctagaggg gatggaagat gcggggagtg   1971
134          agctgggtgg gccctgctag cgagagaggt caaccccggt ggccaggggaa cccacttcca   2031
135          agcgcaggga cgccggcctc cagctggtgt gtgctaaggc tccgtcctga ctgccctgtg   2091
136          ccctggaaaa gcagcaatac atccgcccct tacagccctc tggctagagg agccaccagt   2151
137          ggaaaggaag ccctccatcc tctggtatta acgccttaat gccctgtct tttactgtaa    2211
138          gttacttaga tcattttttgg aagcaggcgt ggtagagtcc tgtaaatgaa tgctctgggc   2271
139          tagatacagc ttggagaacc tgctggcctt gttagacaga acttgggcct ttgccagcag   2331
140          caagaggtga agcgaagcca ctcttacctc tcccttcccc tcccacctgc ccctgcgta    2391
141          ggcacccaga cttggagaga cccgtctgct gttaatactt ccatcctctt ccttcccaaa   2451
142          gagcagatcc caaggcattt actccttggt ctgtctcgct ttatctgtcg ccctcccag    2511
143          cgctgagagc ctcccctggc tgtcagcagc actgtgtcca ggctcttgtc tgaacaccgc   2571
144          agcccctcct tcgctccttc cacagctcag catgtcacgg caaggactgc cgcattggtg   2631
```

```
145        atggagggcc agctgagggg aagttgctgg tgagtttcct ttctccattt ctagcatatg    2691
146        acacctggcc tctgcttgag cacttaggtg acaggaactt ccgcacctcc tgaggccctg    2751
147        gatgattcta attgttagaa attctaattg ttagaaatcc ttccttataa tgaatgaatt    2811
148        ctgctttcct ataatttcta cctattgggc cttgttctgt tctctggaac taaacagaac    2871
149        aaccatttac ccctcctttt caaactagag aataaacatt tggttttaga aaaaaaaaaa    2931
150        aaaaaaaaaa aaaaaaaaaa aaa                                             2954
151  <210> SEQ ID NO 2
152  <211> LENGTH: 567
153  <212> TYPE: PRT
154  <213> ORGANISM: Homo Sapiens
155  <400> SEQUENCE: 2
156        Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu Ala Gln
157        1               5                   10                  15
158        Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr Leu Gly
159                        20                  25                  30
160        Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala Gln Ser
161                        35                  40                  45
162        Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys Arg Arg
163            50                  55                  60
164        His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln
165        65                  70                  75                  80
166        Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His
167                        85                  90                  95
168        Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala Thr Pro
169                        100                 105                 110
170        Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp
171                        115                 120                 125
172        Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys Gln Pro
173            130                 135                 140
174        Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu
175        145                 150                 155                 160
176        Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro
177                        165                 170                 175
178        Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu
179                        180                 185                 190
180        Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu Ala Ala
181                        195                 200                 205
182        Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala
183            210                 215                 220
184        Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys
185        225                 230                 235                 240
186        Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg
187                        245                 250                 255
188        Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg
189                        260                 265                 270
190        Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly
191                        275                 280                 285
192        Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys
193            290                 295                 300
194        Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser
```

```
195        305                  310              315              320
196        Ala Gln Ala Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro
197                        325              330              335
198        Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala
199                        340              345              350
200        Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile
201                    355              360              365
202        Glu Ala Pro Pro Ser Leu Tyr Ser Cys Asp Asp Cys Gly Arg Ser Phe
203            370              375              380
204        Arg Leu Glu Arg Phe Leu Arg Ala His Gln Arg His Asp Thr Gly Glu
205        385              390              395              400
206        Arg Pro Phe Thr Cys Ala Glu Cys Gly Lys Asn Phe Gly Lys Lys Thr
207                    405              410              415
208        His Leu Val Ala His Ser Pro Val His Ser Gly Glu Arg Pro Phe Ala
209                    420              425              430
210        Cys Glu Glu Cys Gly Arg Arg Phe Ser Gln Gly Ser His Leu Ala Ala
211                435              440              445
212        His Arg Pro Asp His Ala Pro Asp Arg Pro Phe Val Cys Pro Asp Cys
213            450              455              460
214        Gly Lys Ala Phe Arg His Lys Pro Tyr Leu Ala Arg His Arg Arg Ile
215        465              470              475              480
216        His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys Ala Phe
217                    485              490              495
218        Ser Gln Lys Ser Asn Leu Val Ser His Arg Arg Ile His Thr Gly Glu
219                500              505              510
220        Arg Pro Tyr Ala Cys Pro Asp Cys Asp Arg Ser Phe Ser Gln Lys Ser
221                515              520              525
222        Asn Leu Ile Thr His Arg Lys Ser His Ile Arg Asp Gly Ala Phe Cys
223            530              535              540
224        Cys Ala Ile Cys Gly Gln Thr Phe Asp Asp Glu Glu Arg Leu Leu Ala
225        545              550              555              560
226        His Gln Lys Lys His Asp Val
227                    565
228    <210> SEQ ID NO 3
229    <211> LENGTH: 378
230    <212> TYPE: DNA
231    <213> ORGANISM: Homo Sapiens
232    <220> FEATURE:
233    <221> NAME/KEY: CDS
234    <222> LOCATION: (1)...(378)
235    <400> SEQUENCE: 3
236        ggt gga gat gcc gtc gac cgc ccc ttc cag tgt gcc tgt tgt ggc aag    48
237        Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys Cys Gly Lys
238        1               5                   10                  15
239        cgc ttc cgg cac aag ccc aac ttg atc gct cac cgc cgc gtg cac acg    96
240        Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg Val His Thr
241                    20                  25                  30
242        ggc gag cgg ccc cac cag tgc ccc gag tgc ggg aag cgc ttt acc aat   144
243        Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg Phe Thr Asn
                        35                  40                  45
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresp nding explanation is presented in the <220> to
<223> fields of each sequence which pres nts at least one n or Xaa.

PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/477,392

DATE: 01/31/2000
TIME: 11:06:53

Input Set: I477392.RAW

Line	?	Error/Warning	Original Text
680	W	"N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe X
682	W	"N" or "Xaa" used: Feature required	Xaa Xaa His Xaa Xaa Xaa His Xaa